Characterization and Application of an External Validation Set for Salmonella Mutagenicity (Q)SAR Models Using Structural Fingerprints of Known Toxicophores

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[The findings and conclusions in this presentation have not been formally disseminated by the FDA and should not be construed to represent any agency determination or policy]

Abstract

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The primary goal of this study was to evaluate how well the S. typhimurium and S. enterica Salmonella mutagenicity test results could be predicted using commercial (Q)SAR models. The study evaluated the performance of three commercially available (Q)SAR models, Leadscope, Hansen K. (Draft Guidance) (2008), and DfW, using external datasets from the scientific literature and FDA approval documents and regulatory documents. The study also evaluated the performance of a new software model, LMA, using a proprietary database of experimental data. The study found that all three models performed well, with sensitivities ranging from 61% to 83% and negative predictivities ranging from 71% to 83%. However, the models showed different levels of performance for different types of chemicals. The study also found that the models were able to correctly identify chemicals with high degrees of red shading, indicating high levels of mutagenicity. Overall, the study found that the models were able to predict the mutagenicity of the chemicals with good accuracy, and that the models were able to be used to identify potentially mutagenic chemicals prior to experimental testing. This can help reduce the number of chemicals that need to be tested experimentally, which can save time and resources.